

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2001, 08:09:20 ; Search time 3038.97 Seconds
(without alignments)
19188.953 Million cell updates/sec

Title: US-09-227-881-3

Perfect score: 6169

Sequence: 1 atcttggtcagtttaccctc.....cttggtccctccatgtcag 6169

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 0%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT	2
BF726094	
LOCUS	BF726094 429 bp mRNA EST 05-JAN-2001
DEFINITION	bx23h10.y1 Human Iris cDNA (Un-normalized, unamplified): Bx Homo sapiens cDNA clone bx23h10 5', mRNA sequence.
ACCESSION	BF726094
VERSION	BF726094.1 GI:12042005
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 429)
AUTHORS	Wistow,G.J., Bernstein,S., Behl,A. and Smith,D.
TITLE	NEIBANK: EST analysis and bioinformatics for ocular genomics invest. Ophthalmol. Vis. Sci. 41 (2000) in press
JOURNAL	Invest. Ophthalmol. Vis. Sci. 41 (2000) in press
COMMENT	Section on Molecular Structure and Function National Eye Institute 6/31, NIH, Bethesda, MD 20892-2740, USA Tel: 301 402 3452 Fax: 301 496 0078 Email: graeme@helix.nih.gov Plate: 23 row: h column: 10 Seq primer: M13P1 reverse primer (ABI). Location/Qualifiers 1. 429
FEATURES	/organism="Homo sapiens" /db_xref="taxon:9606" /clone="bx23h10" /clove_1lb="Human Iris cDNA (Un-normalized, unamplified): Bx" /tissue_type="Iris" /dev_stage="Adult" /lab_host="EMDH10B" /note="Organ: Eye; Vector: pCMVSPORT6; Post-mortem iris tissue was pooled from 10 individuals ranging in age from 4-80 years and RNA was extracted. From this pooled sample an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A directionally cloned cDNA library in the pCMVSPORT6 vector was constructed at Life Technologies, essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adaptor [5'-pGACTAGTCTTGATTCGCAGCGGCCGCC(CT)15-3']. Not I/blunt end inserts were cloned into the Not I/EcoRV sites in the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
BASE COUNT	107 a 129 c 130 g 63 t
ORIGIN	
Query Match	7.0%; Score 429; DB 166; Length 429;
Best Local Similarity	100.0%; Prid. No. 1.7e-65;
Matches 429; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	5383 cagctgtccacgtgctgttcctgcgcctcccgctgctggatgatgttgaggcgaagaagctc 5442
Db	1 CAGGTGTCACAGTGGTCTTTGCGCTCCCTCGTGTTGGGANTGGGGCCACGACAGCTC 60
OY	5443 agctcagaagaagccaabtaacagaaatgccagatgcccaatgcatattactttcagtgtggcagctc 5502
Db	61 AGCTCAGCAAGAAGCCAATACCAGAGTGGCCCATGCGAATTAACTTTCACTGTGGCCAGTCC 120
OY	5503 ccgaatgaatccagctgtcccgagagcagagcagcgacaatgtagtcaatccataacttacaga 5562
Db	121 CCAATGAATCCAGCTGCCCCAGAGCACGAGCCAGGCGCATGTCAATCATTAACCTTAACA 180
OY	5563 gagcacagcagaccaccaaagctcttagacctggaggcgccaccaaaagcttgactcagctccctcg 5622

QY	1321	acctgagctcaatggaacctctgctcccaaggttcaagaatctctctgctcagacctc	1380
DB	293	atcttggctcattggaacctctgctcccaaggttcaagaatctctctgctcagacctc	352
QY	5623	aggagctctccctccacaaattgaaccttggaaccaagctgcccagagagagaccagga	5662
DB	241	AGAGCCTCCCTCCACCAATTTACCTTGGACCAAGCTGCCAGGCCCCACAGAGAGG	300
QY	5683	gagctgcagaaggaagctgagcacccttgagagcaggaagagagagaccagctggaaccaca	5742
DB	301	GGCTGCAGAGAGGAGACTGGGCACTTGAGGGGGAGGAGGACCACTGGAACCCAAACCA	360
QY	5743	gagagttgaggaactgacctacagcaacctctccgagagaaagtcagcttgaggaagaga	5802
DB	361	GAGAGTTGGAGACTGGCTTACAGCAACCTCTCCGAGACAGTCAAGTTCTGTGAGAGAGAGA	420
QY	5803	agaaagcagc	5811
DB	421	AGAAAGCGAC	429
RESULT	3		
LOCUS	AQ057239	660 bp	DNA
DEFINITION	CIT-HSP-2340D14.TF	CIT-HSP	Homo sapiens genomic clone 2340D14, DNA
ACCESSION	AQ057239		
VERSION	AQ057239.1	GI:3353765	
KEYWORDS	GSS.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Mammalia; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Baas,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M., and Venter,J.C.		
TITLE	Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)		
JOURNAL	Unpublished (1998)		
COMMENT	Other GSS: CIT-HSP-2340D14.TF		
	Contact: Mark Adams		
	Department of Eukaryotic Genomics		
	The Institute for Genomic Research		
	9712 Medical Center Dr., Rockville, MD 20850, USA		
	Tel: 301 838 0200		
	Fax: 301 838 0208		
	Email: mdadams@tigr.org		
	Clones are available from Research Genetics (info@resgen.com). BAC		
	Ends are available from Research Genetics (info@resgen.com). BAC		
	http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.		
	Seq primer: M13 Reverse		
	Class: BAC ends.		
FEATURES			
Source	Location/Qualifiers		
	1..660		
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	/db_xref="taxon:9606"		
	/clone="2340D14"		
	/clone_1lb="CIT-HSP"		
	/sex="Male"		
	/cell_type="Sperm"		
	/note="Vector: pBeloBAC11; site_1: HindIII; site_2: HindIII"		
BASE COUNT	116 a 188 c 150 g 206 t		
ORIGIN			
Query Match	2.9%;	Score 180.8;	DB 223; Length 660;
Best Local Similarity	86.0%;	Pred. No. 5.9e-22;	
Matches 215; Conservative	0;	Mismatches 27;	Indels 8; Gaps 1

DB	Accession	Source	Organism	Reference Authors	Title	Journal Comment
OY	1381	CG979787/c	LOCUS	DEFINITION	AO379787	539 bp DNA
OY	1433	gagatgggtttccatattatgacccggctggtcttgaactccctgacctgaagtgatca	1432			
DB	353	CACGACTGCTGGGATTACAGCGCCACACACCACCCCGGCTAATTTTGTATTTTAA	412			
OY	1433	gagatgggtttccatattatgacccggctggtcttgaactccctgacctgaagtgatca	1492			
DB	413	GAGATGGGTTTACACAGATGTGGCCAGGCTGTCTGCACACTCCCGACCTCAGGATCA	472			
OY	1433	cccaactgaagctctctaaagtgtctggtgattacagcatgcatcgcgcgcgcgaag	1552			
DB	473	CCCACTGCTGCTCCCAAGTGTGGGATTAACAGGCTGTGGCCACTGCGCCACGCTAAT	532			
OY	1553	gtcagtgctt 1562				
DB	533	TTTTGTATT 542				
RESULT 4	AO379787/c	LOCUS	DEFINITION	AO379787	539 bp DNA	GSS 20-MAY-1999
VERSION	AO379787	KEYWORDS	AO379787.1	GI:4350810		
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.					
	1 (bases 1 to 539)					
	Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter					
	, J.C.					
	Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready					
	Map Building					
	Unpublished (1997)					
JOURNAL	Contact: Shaying Zhao, William Nierman, Mark Adams					
COMMENT	Department of Eukaryotic Genomics					
	The Institute for Genomic Research					
	9712 Medical Center Dr., Rockville, MD 20850					
	Tel: 301 838 0200					
	Fax: 301 838 0208					
	Email: hbe@tigr.org					
	Clones are derived from the human BAC library RPCI-11. For BAC					
	library availability, please contact Pieter de Jong					
	(pieterdejong.med.bufiled.edu). Clones may be purchased from					
	BACPAC Resources (http://bacpac.med.bufiled.edu/ordering) or from					
	Research Genetics (info@resgen.com). BAC end search page:					
	http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html					
	Seq primer: SP6					
	Class: BAC ends.					
FEATURES	Location/Qualifiers					
SOURCE	1..539					
	/organism="Homo sapiens"					
	/db_xref="GDB:7558034"					
	/db_xref="taxon:9606"					
	/clone="RPCI-11-152C3"					
	/clone_lib="RPCI-11"					
	/sex="Male"					
	/cell_type="lymphocytes"					
	/note="vector: pBAC3.6; site_1: EcoRI; site_2: EcoRI;					
	RPCI11 Human Male BAC Library"					
BASE COUNT	187 a 112 c 123 g 116 t 1 others					
ORIGIN						
Query Match	2.9%	Score 179.8;	DB 227;	Length 539;		
Best Local Similarity	76.8%	Pred. No. 9e-22;				
Matches 235;	Conservative 0;	Mismatches 63;	Indels 8;	Gaps		
OY	1280	aggatggaggtctgtgtctacactactctgtatgctctacactgagctcactgcacac	1339			
DB	327	AGAGTCGCTGTCACACNAGGTGGAGTTCACTGGCGGGGATCTGGGCTACATGCAAC	268			

OY	1340	tcgcctcccaaggtcgaagaattctctcgtctcccaagctcccgcgtagctggactacaag	1399
Db	267	TTCTGCTTCCTCCGGGTTTCAAGCAATTCTCTGCTCCCTACGCTCCGAGTAGCTGGACACAG	208
OY	1400	gc-----gcacggcccgctaatttctgattctgtagaagatgaggtttccacata	1451
Db	207	GCATGTGCACACATACCCCGGCTAATTTTTGTATATTTTATGAGAAACGGGGTTTCACATG	148
OY	1452	ctaacccgctgctgtctgaactctcctgaactcaagtgatccaccacactcagctctcaa	1511
Db	147	TTGGCAGAGCTGCTGTTGAACCTCCTGACCTCAGAGTGATCACAGACCTTGCCCTCTAAA	88
OY	1512	gtgtctggattacaaggcatgaatgctaccggccggccgaaggtctagtgtttaataagaa	1571
Db	87	GTGCTGGATTACAGAGCTAGTCACACACCGCCGCGCTCAATATCCCTTTTTCACAGCTCA	28
OY	1572	taactt 1577	
Db	27	TGATTT 22	
RESULT	5		
LOCUS	A2520729	613 bp	DNA
DEFINITION	RPC1-11-7965.TJ.D RPC1-11 Homo sapiens genomic clone RPC1-11-7965, DNA sequence.		
ACCESSION	A2520729		
VERSION	A2520729.1	GI:108333239	
KEYWORDS	GSS.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 613)		
AUTHORS	Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter J.C.		
TITLE	BAC end sequences of library RPC1-11		
JOURNAL	Unpublished (1997)		
COMMENT	Other_GSSs: RPC11-7965..TJ RPC11-7965..TV Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel.: 301 838 0200 Fax: 301 838 0208 Email: szhao@tigr.org Clones are derived from the human BAC library RPC1-11. For BAC library availability, please contact Pieter de Jong (pieter@jeong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html This BAC end was generated during the Rad process and may have higher chance of clone tracking errors. Seq primer: Sp6 Class: BAC ends. Location/Qualifiers 1..613 /organism="Homo sapiens" /db_xref="GB:"7530100" /db_xref="taxon:9606" /clone="RPC1-11-7965" /clone_1ib="RPC1-11" /sex="Male" /cell_type="Lymphocytes" /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPC11 Human Male BAC library"		
BASE COUNT	153 a	134 c	141 g
ORIGIN	185 t		
Query Match	2.9%	Score 179,	DB 245,
Best Local Similarity	76.4%	Pred No. 1,2e-21;	Length 613;

	Matches	236;	Conservative	0;	Mismatches	65;	Indels	8;	Gaps	1.
OY	1280	agggaggaaggtcgtgtgtcttaacacttaacgtatgcttaacactgaagctcaacgaacc	1339							
Db	118	AGAGGCTTGGCTTTGTGGGCCACAGCTGGAGTACAGTGTCGATGTGCAGTCACTCAAC	177							
OY	1340	ctgtgctccaggtctcaagaatcttcctgtcttaagccctccggtagcttgtaactaag	1399							
Db	178	TCTGACTCTCTGGTTCAAGACATTTCTCTGTCTTAGCCCCCGAATTAGCTGGGATTACG	237							
OY	1400	gcg-----caagccggactaattcttgatacttgtaagtagaga tggaggtctcaacata	1451							
Db	238	GTGGCTGCACACATGCGCTACGTAATTTGTGTATTTTTAGCAAGATGGGGTTTCACATA	297							
OY	1452	ctagccggcgctggtcttgaaactcttgacctcaagtgatcaccaccaactcaagctctaa	1511							
Db	298	TTGGTCAGAGCTGTGTGGAACTCTGACCTCAGTGATGCACCCGCTTCAGCTCCCAA	357							
OY	1512	gtgctggagattacagcatatgctaacccgcccggcccaaggtctgcttctaataagaa	1571							
Db	358	GTGGCTGGGATTTACAGAGCGTGAACCCAGCCAGCTGCTGTGTCCAGGGGTATGTTTTATAGAA	417							
OY	1572	taactctgaa 1580								
Db	418	TAAATTCGA 426								

RESULT	6	
LOCUS	AO636457/c	
DEFINITION	AO636457 645 bp DNA	GSS
ACCESSION	RPCT-11-465121.TU	RPCT-11 Homo sapiens genomic clone RPCT-11-465121
VERSION	AO636457	DNA sequence.
KEYWORDS	AO636457.1	GI:5099092

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 645)

J.C.

JOURNAL
COMMENT

Unpublished (1997)
Contact: Shaying Zhao, William Niernan, Mark Adams

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
tel. 301 839 0300

Tel.: 301 838 0200
 Fax: 301 838 0208
 Email: hbeet@igf.org
 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACSPC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genet cs (<http://resgen.com>). BAC end search page: http://www.igf.org/cdb/hungen/bac_end_search/bac_end_search.html
 Seq primer: Sp6
 Class: BAC ends.

FEATURES	Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="GDB:767838"
/db_xref="taxon:9606"
/clone="RPCI-11-465I21"
/clone_lib="RPCI-11"
/seq="ttst1"
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/cell_type="Lymphocytes"
/notes="Vector: pBACe3.6; Site1: EcoRI; Site2: EcoRI
RCIII Human Male BAC Library"
BASE COUNT      214 a      118 c      139 g      174 t
ORIGIN

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Query Match	2.9%	Score 179;	DB 231;	Length 645;
Best Local Similarity	88.2%;	Pred. No. 1.2e-21;		
Matches 209;	Conservative 0;	Mismatches 20;	Indels 8;	Gaps 1;

Y 1322 cctgagcctaactgaacctgcctccagglttaagcaattctctgttccaagctccc 1381
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
248 CTTTCAAGCTCCTGCAACCTCTGGCCCTTCAGGTTCATTAATTCTCTGCCTCACCTCCC 189

Y 1382 gcgtacgtggactacagcg-----cacgccgctaatttgtatcgttag 1433

188 GAGTACTGGATTACAGGCGTGTCTACCACCGCCAGCTAATTTTGTATTTTAGTAG 129

128 AGATGGGATTTCCACCATGTTGGCCGCGGTGGTCTTCGCACTCCGACCTCAAGATCTGC 69
1434 agatggggtttccaccatattagcccggtgtgtcttgaactcccgacctcagtgatccac 1493

1494 ccaccctcagcctctctaaagtctgtagattacagcatgagtcaccgcgcgcgcca 1550

b
68 CCACCTCAGCCTCCCAAGTGTGTGGATTACAGCATGAGCCACCGCGCCGCCCA 12

RESULT 7
0387027/C

	678 bp	DNA	GSS	21-MAY-1999
LOCUS	AQ387027			
DEFINITION	RPC111-153C12.T1	RPC1-11 Homo sapiens genomic clone	RPC1-11-153	

CCESION
DNA sequence.
AQ387027
AQ387027.1 GI:4358050

KEYWORDS	GSS.
SOURCE	human.
ORGANISM	Homo sapiens

Chordata; Craniata; Vertebrata; Euteleostom
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
1 (bases 1 to 678)
Zhao, S., Adams, M.D., Niernan, W., Malek, J., de Jong, P. and Vente, J.C.

TITLE	Use of BAC End Sequences from Library RPCI-11 for Sequence-Read Map Building
JOURNAL	Genomics
VOLUME	10
NUMBER	1
PAGES	1-10
DATE	1997
DOI	10.1006/geno.1997.2501
ISSN	0888-7543
KEYWORDS	BAC end sequences, sequence mapping, genomic libraries, RPCI-11, BAC clones, sequence analysis, map building, genomic mapping, BAC clones, sequence analysis, map building, genomic mapping
ABSTRACT	The BAC end sequences (BESs) of a genomic library can be used to map the library. The BESs can be used to map the library to a reference map, to map the library to a physical map, or to map the library to a genetic map. The BESs can be used to map the library to a reference map, to map the library to a physical map, or to map the library to a genetic map. The BESs can be used to map the library to a reference map, to map the library to a physical map, or to map the library to a genetic map.

unpublished (1997)
Other-GSSs: RPC11-153C12.TV
Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850

Tel: 301 838 0200
Fax: 301 838 0208

Email: indoe@lrgi.org
Clones are derived from the human BAC library RGT-11. For BAC library availability, please contact Pieter de Jong

(pete@edejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genetics (info@resgen.com). RAG and search page:

http://www.tigr.org/tdb/humgen/bac_end_search.htm
Seq primer: SP6

FEATURES	Class: BAC ends.
source	Location/Qualifiers
	1. .678

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/organism="Homo sapiens"  
/db_xref="GDB:7558437"  
/db_xref="taxon:9606"
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/usb_l1b="CA001:5000
/clone="RPci-11-153c12"
/clone_l1b="RPci-11"

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/sex="Male"
/cell_type="Lymphocytes"
/notes="Vector: pRACE3.6: Site 1: EcoRI. Site 2: EcoRI."

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BASE COUNT	RPC111 Human Male BAC Library			
	210 a	151 c	171 g	146 t
210 a	151 c	171 g	146 t	

Query Match	Score	DB	Length
2.98;	179;	227;	678;

Db	66	CCACCTCCCAATTCAAGGATTCTCTGCTCCAGCTCTCCAGTAGAGCGGATTACAG	125
Oy	1401	cg-----cagccgcgcgaattcttgatgtatgtatgataagatgagggatccacatat	1452
Db	126	TGCCCAACCAACACACCACTCACTAATTTTGTATTTTAGTAGAGATGGGTTTCACCATAT	185
Oy	1453	tggccgcgcgttgctcttgaactctcgaactcaagtgatccaccacactcaagctctctaag	1512
Db	186	TGGCAGAGTGGTCTTCGAATCTCTCAACCTCAAGTGATTCACCCGGCTCAGCTCCACAGAG	245
Oy	1513	tgcctggattacaaggaatgatgcacgcgcgcgcgaagggatgctgttaataagaaat	1572
Db	246	TGCTGGGATATTATAGGCGGTAGCCACCGCGCGCTTGCGACAGGTCTTTTAAGAGAAAG	305
Oy	1573	aa 1574	
Db	306	aa 307	

RESULT	10
AQ112451	
LOCUS	
DEFINITION	AQ112451 516 bp DNA GSS 29-AUG-1998
ACCESSION	CIT-HSP-2372C9.TF CIT-HSP Homo sapiens genomic clone 2372C9, DNA sequence.
VERSION	AQ112451
KEYWORDS	AQ112451.1 GI:3484611
SOURCE	GSS.
ORGANISM	human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 516) Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C. Use of a random human BAC End Sequence Database for Sequence-Ready Map Building Unpublished (1998) Other-GSS: CIT-HSP-2372C9.TR Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: mdadams@tigr.org Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html . Seq primer: M13-21 Class: BAC ends.
JOURNAL	
COMMENT	

FEATURES	source	Location/Qualifiers
		1. .516
		/organism="Homo sapiens"
		/db_xref="taxon:9606"
		/clone="2372C9"
		/clone_11b="CIT-HSP"
		/sex="Male"
		/cell_type="Sperm"
		/note="Vector: pBelobAC11; Site_1: HindIII; Site_2: HindIII"
BASE COUNT		87 a 145 c 118 g 166 t
ORIGIN		

Query Match	2.9%	Score 177.6:	DB 224:	Length 516:
Best Local Similarity	85.2%	Pred. No. 2.2e-21:		
Matches 213:	Conservative	0:	Mismatches 22:	Indels 8:
				Gaps
Qy	1321	actctggacgtcactgcgaacccctcttcctcccaagtttcgaagaatctccctcgtctctcagctctcc	1380	
Db	255	ATCTCAGCTCAGCTGCACCACTCTCCCTCCCGGGGTCAAGAGGATTCTCCGTCTGCACGCCCTCC	314	

[illegible]

RESULT	11
LOCUS	AO265389/c
DEFINITION	AO265389 577 bp DNA GSS 27-OCT-1998
ACCESSION	CITR1-El-2509010.TF
VERSION	CITR1-El Homo sapiens genomic clone 2509010, DNA sequence.
KEYWORDS	AO265389
SOURCE	AO265389.1 GI:3793589 GSS.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi; Mammalia: Eutheria: Primates; Catarrhini: Hominoidea: Homo. 1 (bases 1 to 577) Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
TITLE	Use of a random human BAC End sequence Database for Sequence-Ready Map Building
JOURNAL	Unpublished (1998)
COMMENT	Other:GSS: CITR1-El-2509010.TR Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: mdams@tigr.org Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html . Seq primer: M13-21 Class: BAC ends.

FEATURES	source	location/Qualifiers
	1. .577	
		/organism="Homo sapiens"
		/db_xref="taxon:9606"
		/clone="2509010"
		/clone_lib="CfTBI-E1"
		/sex="male"
		/cell_type="sperm"
		/note="vector: pBeloBAC11, Site_1: EcoRI; Site_2: EcoRI; Caltech Human BAC Library D"
BASE COUNT	167 a	137 g 146 t
ORIGIN		

	Query Match	2.9%	Score 177.4	DB 226	Length 577
	Best Local Similarity	75.1%	Pred. No. 2.4e+21		
	Matches 238; Conservative	0;	Mismatches 71;	Indels	Gaps 1;
QY	1321	accgagctcactcaaccttgcctcccgagttaagaacatcttcctgtctccaqcttc	1380		
Dd	368	ATTCGCGCTCACTGTGAACCTCTGCCTCCCAAGTTTAAAGTGATTCTCCTGCCCTCAAGCTTC	309		
QY	1381	cgcgtagcttggnachacagc-----gaacgcgccgcctaattttgatattgaaA	1432		

Accession	Sequence	Position
Db	CGAGATCTAGACTACAGGACCCGCCACCAACCGTCGGCAATTTTCGATATTTTAGTA	249
308		
Oy	gagttgggtgttccacatataagccggcctggtcttgaactcttgacctaaagtgtacaa	1492
1433		
Db	GAGACGGGGTTTACCAATGTTGGTCAGAGCTGGTTTAACTCCTGACCTCAGCGGATCCA	189
248		
Oy	cccaactcagcctctctaaagtgtctgggattcaagcattgaactccgctggccggccaag	1552
1493		
Db	CCCCCTTGGGCTCCCAAGTGTGGGATTTACAGGCAATGAGCCACTGCACCCAGCCAGA	129
188		
Oy	gtcacgtgttcaataaggaataacttgaatgtgttcaactcaaaccaaggaagaacagacaa	1612
1553		
Db	GATACATTTTGTGAATCTAGACGTGAGTCTAGTGCAGACAGCTCTCCACAGCAAGGAAAT	69
128		
Oy	agctgtgataatttcag	1629
1613		
Db	AGTAATACGTGATGAG	52
68		

RESULT	12
LOCUS	A1583291/c
DEFINITION	A1583291 548 bp mRNA EST 14-DEC-1999
ACCESSION	U55602.x1 NCI-GAGE-HSC4 Homo sapiens cDNA clone IMAGE:2244818 3' similar to FR:013538 Q13538 ORF2: FUNCTION UNKNOWN. ; contains Alu repetitive element.; mRNA sequence.
VERSION	A1583291
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE 1 (bases 1 to 548)
AUTHORS NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.

CDNA Library Preparation: David B. Kitzman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAC clone distribution Information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bdrrp/image/image.html
Insert length: 664 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 464
POLYA-No.

FEATURES	SOURCE
Location/Qualifiers	
1. .548	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="IMAGE:2244818"	
/clone_1lb="NCI-CD34+ HSC4"	
/tissue_type="CD34+ , CD38-	from normal bone marrow donor
/lab_host="DH10B"	
/note="Organ: bone marrow; Vector: pAMP1; mRNA made from lymphoid tissue, cDNA made by oligo-dT priming. Directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified. cDNA library preparation: David B. Kitzman, Ph.D. Reference: Kitzman et al. (1996) Cancer Research 56:5380-5383."	
BASE COUNT	150 a 136 c 129 g 133 t
ORIGIN	

Query Match	2.98;	Score 177.2;	DB 22;	Length 548;
Best Local Similarity	78.88;	Pred. No. 2.6e-21;		

Matches	227	Conservative	0	Mismatches	53	Indels	8	Gaps	1
QY	1277	gtgaggtgtgaggtgtctgtcttaacactactctgtatgctcttaacccgaggtactctga							1336
Db	546	GAGGAGATCTTGATCTTGATCTGCTCAGGCGTGGAGATGAGTGGCATGTGCTGCTACTGCA							487
QY	1337	aacctgtgctcccgaggtctcaagcaattctctctgtctcagcctcccgctgaactgtgactta							1396
Db	486	ACCTCGGCTCTCAGAGTTTCAAGCATTTCTCCGCTCAGCCCTCTGAGCAGCTGAGACTA							427
QY	1397	cagggg-----caagcccgcgcaattttgtatctgtttgtaagaattgggtctcaac							1448
Db	426	CAGGGCGCCCGCCACACACGCTGGCTAAATTTTGTATTTTAAAGATAGAGGGGTTTCAAC							367
QY	1449	atatattgcgcgggtgtgtctttaaaccctcgtgaacctcaagttgatactcaaccacactaaacctct							1508
Db	366	ATGTGGGCGACAGCTGTGCTGGAATCTGAGACTCTCAGGTGATGCACCCACACTTGTGCTCC							307
QY	1509	aaagtgctgggagatatacaagcataagatacaacggcccgccggaagggtca							1556
Db	306	AAAGTGTCTGGGATTTCAGAGCATGAGCCACCGCTGCCACGCCCAAGATTTAA							259

RESULT	13				
BF920612/c					
LOCUS	BF920612	400 bp	mRNA	EST	19-JAN-2001
DEFINITION	OVO-NT0151-081100-455-104 NT0151			Homio sapiens	CDNA, mRNA sequence.
ACCESSION	BF920612				
VERSION	BF920612.1			GI:12316500	
KEYWORDS	EST.				
SOURCE	human.				

REFERENCE
1 (bases 1 to 400)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663
COMMENT	Contact: Simpson A.J.G.

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel.: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?LI-QV0&t2-QV0-NT0151>)
 081100-455-f04e3-2000-11-08&t4-1)
 Seq primer: puc 18 forward
 High quality sequence start: 4
 High quality sequence stop: 400.
 Location/Qualifiers
 1..400

/note="Organ: nervous_tumor; Vector: puc18; Site_1: Sma1;
 Site_2: Sma1; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

Db	CCACCTCCCAAGGTTCAAGCAATTCTCTGTCACAGCTCTTAAGTAGCTGGGACTAGAG	251
Oy	1401 cgcacg-----cccgctaaatttggatattgttagtaagatagggtttcaacatat	1452
Db	252 GGCCCCGCCACCATACCAAGTAAATTTTCTAATTTTAAAGATAGAGGGGTTTCAACCAT	311
Oy	1453 tggccgctcgtgctcttgaactccctgaacctcaagtgatccaccacactcaagcctcctaag	1512
Db	312 TGTGTACAGCTGTGCTTGAACTCTGTGACCTACAGTGTATCCACCGGCTTTGGCTCCCAAG	371
Oy	1513 tctcggattcaacggcctagtcacacgcccgcgccaagagtgctgttaataaagaat	1572
Db	372 TGTGTGGATGACAGGCGTGAAGCCATGCGCCACGCAACAAGTTTCGAATTTTAAAGCAA	431
Oy	1573 aacttgatggcttactcaaacacacgggaagaacagcaagaactg	1617
Db	432 AATATATATCTATTTAACCTCAATGCAATTCTCAACAGCATG	476

Search completed: November 8, 2001, 12:56:07
Job time: 17207 sec

